

THE FUNCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR-B IN THE HEART

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Academic dissertation



Helsinki University Biomedical Dissertations No. 189

*To be publicly discussed, with the permission of the Faculty of Medicine
of the University of Helsinki, in Lecture Hall 3, Biomedicum Helsinki,
Haartmaninkatu 8, Helsinki, on November 29, 2013 at 1 p.m.*

Helsinki 2013

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ISBN: 978-952-10-9397-5 (nid.)
ISBN: 978-952-10-9398-2 (pdf)
ISSN: 1457-8433
<http://ethesis.helsinki.fi>
Unigrafia

To my mother

*To arrive where you are, to get from where you are not,
You must go by a way wherein there is no ecstasy.
In order to arrive at what you do not know
You must go by a way which is the way of ignorance.
In order to possess what you do not possess
You must go by the way of dispossession.
In order to arrive at what you are not
You must go through the way in which you are not.
And what you do not know is the only thing you know
And what you own is what you do not own
And where you are is where you are not.*

- T.S. Eliot, "East Coker"

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ABBREVIATIONS

| | |
|----------------|---|
| AAV | adeno-associated virus |
| AMPK | adenosine monophosphate-activated protein kinase |
| α SMA | smooth muscle α -actin |
| ATP | adenosine triphosphate |
| Bmx | bone marrow kinase in chromosome X |
| CD | cluster of differentiation |
| CMC | cardiomyocyte |
| CT | computed tomography |
| DAG | diacylglycerol |
| Dll | delta-like ligand |
| E | embryonic day |
| EC | endothelial cell |
| EGF | epidermal growth factor |
| eNOS | endothelial nitric oxide synthase |
| ERK | extracellular signal-regulated kinase |
| FATP | fatty acid transport protein |
| FDR | false discovery rate |
| Flk | fetal liver kinase |
| Flt | fms-like tyrosine kinase |
| GSK-3 β | glycogen synthase kinase-3 β |
| HIF | hypoxia-inducible factor |
| Ig | immunoglobulin |
| iNOS | inducible nitric oxide synthase |
| IP3 | inositol triphosphate |
| K14 | keratin-14 |
| KDR | kinase insert domain receptor |
| MAPK | mitogen-activated protein kinase |
| MEK | MAPK/ERK kinase |
| MCP | monocyte chemotactic protein |
| MHC | myosin heavy chain |
| MI | myocardial infarction |
| MMP | matrix-metalloproteinase |
| mTOR | mammalian target of rapamycin |
| mTORC | mTOR complex |
| NFAT | nuclear factor of activated T-cells |
| NO | nitric oxide |
| NRP | neuropilin |
| PAI | plasminogen activator inhibitor |
| PDGF | platelet-derived growth factor |
| PECAM | platelet endothelial cell adhesion molecule |
| PET | positron emission tomography |
| PGC-1 α | peroxisome proliferator-activated receptor- γ coactivator-1 α |
| PI3K | phosphoinositide 3-kinase |
| PKC | protein kinase C |
| PLC | phospholipase C |
| PIGF | placenta growth factor |
| RECA | rat endothelial cell antigen |
| SD | standard deviation |
| SDS-PAGE | sodium dodecyl sulfate polyacrylamide gel electrophoresis |
| SEM | standard error of the mean |
| SMC | smooth muscle cell |
| sVEGFR-1 | soluble VEGFR-1 |
| TG | transgenic |
| Tie | tyrosine kinase with immunoglobulin and EGF homology domains |
| VEGF | vascular endothelial growth factor |
| VEGFR | VEGF receptor |
| WT | wildtype |

LIST OF ORIGINAL PUBLICATIONS

This thesis is based on the following original publications, referred to in the text with their assigned roman numerals:

- I Kärpänen, T.*, **Bry, M.***, Ollila, H.M., Seppänen-Laakso, T., Liimatta, E., Leskinen, H., Kivelä, R., Helkamaa, T., Merentie, M., Jeltsch, M., Paavonen, K., Andersson, L.C., Mervaala, E., Hassinen, I.E., Ylä-Herttuala, S., Oresic, M., and Alitalo, K. Overexpression of vascular endothelial growth factor-B in mouse heart alters cardiac lipid metabolism and induces myocardial hypertrophy. *Circulation Research* 103(9):1018-26 (2008).

- II **Bry, M.**, Kivelä, R.*, Holopainen, T.*, Anisimov, A., Tammela, T., Soronen, J., Silvola, J., Saraste, A., Jeltsch, M., Korpisalo, P., Carmeliet, P., Lemström, K.B., Shibuya, M., Ylä-Herttuala, S., Alhonen, L., Mervaala, E., Andersson, L.C., Knuuti, J., and Alitalo, K. Vascular endothelial growth factor-B acts as a coronary growth factor in transgenic rats without inducing angiogenesis, vascular leak, or inflammation. *Circulation* 122(17):1725-33 (2010).

- III Kivelä, R., **Bry, M.**, Robciuc, M.R., Taavitsainen, M., Silvola, J., Saraste, A., Hulmi, J.J., Räsänen M., Anisimov, A., Eklund, L., Hellberg, S., Hlushchuk, R., Zhuang, Z.W., Simons, M., Djonov, V., Knuuti, J., Mervaala, E., and Alitalo, K. VEGF-B-induced vascular growth leads to metabolic reprogramming and ischemia resistance in the heart. *Submitted*.

*These authors contributed equally to the study.

ABSTRACT

Despite intensive efforts, vascular growth factors have not yet provided significant help in the treatment of cardiovascular disease. This is likely to change as we gain a better understanding of the underlying biology of these growth factors as well as of their regulation and functions. Members of the vascular endothelial growth factor (VEGF) family are major regulators of blood and lymphatic vessel development and growth. VEGF is essential for vasculogenesis and angiogenesis, whereas VEGF-C is required for lymphatic development. The functions of VEGF-B, one of the younger members of the VEGF family, have however remained largely enigmatic.

This study was undertaken in order to elucidate the role of VEGF-B in the regulation of myocardial and vascular function in the heart, a site of high endogenous expression, as well as its therapeutic potential. For this end, VEGF-B was first overexpressed in the mouse heart, before proceeding to a larger transgenic rat model better suited for studies of cardiovascular physiology. VEGF-B overexpression did not cause overt angiogenesis but led to an increase in the size of capillaries in the heart. Surprisingly, VEGF-B also increased the size of cardiomyocytes, resulting in myocardial hypertrophy. The transgenic animals had significantly lower blood pressure and heart rate than their wild type littermates, and the isolated transgenic mouse hearts seemed to perform better following short-term ischemia-reperfusion.

Strikingly, in addition to myocardial growth, in rats VEGF-B induced impressive growth of the epicardial coronary arteries and their myocardial branches, which was associated with protection from myocardial infarction *in vivo*. However, in skeletal muscle and in the skin, VEGF-B did not significantly induce blood vessel growth, indicating that the heart is a site for specific effects of VEGF-B. These findings indicate that VEGF-B can act as a growth factor for cardiac vessels, which could have significant potential for therapeutic applications in cardiac insufficiency and/or ischemia. Importantly, compared with VEGF and placenta growth factor (PlGF), VEGF-B induced very little vascular permeability or inflammation.

The roles of the VEGF-B receptors, VEGFR-1 and neuropilin (NRP)-1, were also investigated, and the tyrosine kinase domain of VEGF receptor-1 (VEGFR-1) was found to be required for the cardiac hypertrophy induced by VEGF-B. NRP-1, however, did not seem to be involved in these effects. Interestingly, VEGF-VEGFR-2 signaling played a role in the cardiac vessel growth induced by VEGF-B.

In contrast to a prevailing theory, VEGF-B did not increase fatty acid uptake in the heart in our models. Instead, VEGF-B seems to play a role in fine-tuning cardiac metabolism to meet energy demands during for example cell growth. Overall, VEGF-B has potential as a therapeutic growth factor in the ischemic heart, as it induces coordinated effects on cardiac blood vessels and cardiomyocytes, ultimately protecting the heart from ischemia.

REVIEW OF THE LITERATURE

Introduction

Ischemic heart disease is the leading cause of death in the modern world, encompassing over seven million deaths per year according to the latest Global Burden of Disease Update of the World Health Organization (World Health Organization, 2008). Angina pectoris symptoms were first systematically described by William Heberden in 1772 (Heberden, 1785), with only isolated cases documented prior to this. This was followed by pathological studies by British scientists who initially described the theory of myocardial ischemia, which however was not fully accepted until over a century later (Proudfit, 1983). During the eighteenth and nineteenth centuries, the condition was rare, and it only became more significant during the early twentieth century, probably due to evolving changes in lifestyle, as first hypothesized by Michaels in 1966 (Michaels, 1966).

Collateral vessels were first described in the human heart in the mid-seventeenth century (Lower, 1669), but considerable controversy about their existence in the normal heart ensued. Post-mortem imaging techniques of animal and human hearts have been developed since the nineteenth century (Spalteholz, 1907; Gross, 1921; Seiler, 2009), and structural coronary anastomoses could be unequivocally visualized in the early 1960's by William Fulton with a novel radiographic technique which permitted visualization of coronary arteries down to fifteen micrometers in diameter (Fulton, 1963a; Fulton, 1963b). Fulton and others were also able to observe not only superficial anastomoses, but also a vast subendocardial arterial plexus arising directly from epicardial arteries (Fulton, 1964) with implications in subendocardial ischemia (Hoffman and Buckberg, 1975), and which could be considerably enlarged in coronary artery disease. Most importantly, the discovery of the existence of structural coronary intercommunications in normal hearts underscored that only their enlargement would be needed for the development of the larger anastomoses found in coronary disease (Fulton and van Royen, 2004).

These observations have led to studies concerning the mechanisms and stimuli behind coronary vessel formation, since although revascularization of stenotic coronary arteries combined with pharmaceutical therapy is still the standard therapy for coronary artery disease, some patient groups respond poorly to these treatments, and the mortality benefit is not clear (Adamu et al., 2010). Therefore, new therapeutic strategies for promoting collateral artery formation, or arteriogenesis, are needed, as well as novel treatments for improving myocardial function. Studies of potential growth factors mediating coronary vessel growth have invariably overlapped with angiogenesis research in for example tumor biology and embryology; thus it is important to review these in the same context.

1. The cardiovascular system

The blood vascular system consists of the heart and a hierarchical network of blood vessels. The heart pumps oxygenated blood first *via* the aorta and major arteries to smaller arterioles and capillaries, where diffusion of oxygen, nutrients and waste products is possible. The deoxygenated blood is then delivered back to the heart *via*

venules and veins and from there to the lungs, where respiration, ventilation and reoxygenation of the blood occur.

1.1. Development of the blood vascular system

This blood circulatory system is the first organ system to develop and appears during the third week of development in the human embryo when passive diffusion of nutrients and waste products becomes insufficient for development (Sadler, 2006). Vasculogenesis, referring to the initial formation of the primitive vascular plexus, begins when hemangioblast progenitors of mesodermal origin migrate and differentiate to form primary blood islands, from which both hematopoietic cells and angiogenic endothelial cell (EC) precursors are formed (Risau and Flamme, 1995). The primitive vascular plexus is subsequently remodeled into a network consisting of arteries, veins, and capillaries of different sizes, and the vessels are stabilized by recruited mural cells, or pericytes and smooth muscle cells (SMCs). Among the most extensively established arterial and venous cell surface markers expressed during early stages of arterial-venous differentiation are the membrane-bound ephrin-B2 ligand and the EphB4 receptor, respectively (Wang et al., 1998).

Angiogenesis, or the process of blood vessel formation from pre-existing vessels, occurs through either sprouting or intussusception (splitting) (see also Risau, 1997; reviewed in Chung and Ferrara, 2011). Vascular endothelial growth factor (VEGF) and its receptors are essential for the early development of the vasculature, whereas later stages of vascular remodeling require for example the angiopoietins and their Tie receptors for maintenance of vascular integrity (reviewed in Saharinen et al., 2010).

Angiogenesis occurs subsequently in the fully developed adult organism during for example wound healing, in the endometrium throughout the menstrual/estrous cycle, in pregnancy, as well as in inflammation and skeletal muscle growth. In addition, angiogenesis plays an important role in several pathological conditions such as cancer and atherosclerosis, as well as in ocular pathologies such as age-related macular degeneration and diabetic retinopathy (Chung and Ferrara, 2011).

1.2. Development of the coronary vasculature

The embryonic origin of coronary ECs is still subject to considerable controversy. One traditional theory involves the proepicardial organ, a transient mesothelial cell structure situated on the surface of the embryonic heart from which epicardial precursors arise. Coronary SMCs and myocardial fibroblasts are thought to be mostly derived from epicardium-derived cells *via* epithelial-to-mesenchymal transition, migrating into the heart along with the epicardium (Mikawa and Gourdie, 1996; Dettman et al., 1998; Vrancken Peeters et al., 1999). A population of coronary ECs has been reported to arise from proepicardial precursors at least in avian embryos (Perez-Pomares et al., 2002). However, more recent studies suggest that the proepicardium is not a major source of ECs (Winter and Gittenberger-de Groot, 2007; Cai et al., 2008).

Interestingly, a novel theory on coronary EC origin has recently been presented in mice, where coronary vessels were shown to sprout from the sinus venosus, the venous endothelial cavity returning blood to the embryonic heart (Red-Horse et al., 2010). In addition, in this study a small population of coronary ECs was shown to originate from

the endocardium, a theory which has also previously been presented although never before supported by clonal analysis (Viragh and Challice, 1981).

1.3. New insights into ischemic heart disease

It has hitherto been generally accepted that ischemic heart disease is pathophysiologically caused by atherosclerotic plaques causing arterial stenosis, although in many patients the severity of symptoms do not correlate with the grade of obstruction. It has recently been suggested that in treating cardiac ischemia, one should not only concentrate on obstructive disease of the coronary arteries themselves, but also on abnormalities of coronary microcirculation, endothelial dysfunction, spontaneous thrombosis and inflammation, all causing dysregulation of blood vessel–cardiomyocyte interactions and capable of leading to myocardial ischemia (Lanza and Crea, 2010; Marzilli et al., 2012). Indeed, novel therapies should perhaps focus on mechanisms which could improve the survival of the cardiomyocytes themselves, regardless of the underlying cause of ischemia.

1.4. Arteriogenesis

Arteriogenesis, a name first proposed by Wolfgang Schaper and colleagues at the end of the twentieth century (Schaper et al., 1999), distinguishes capillary sprouting (angiogenesis) from the growth of collateral vessels able to perfuse an area whose supplying artery has been occluded (Schaper and Schaper, 2004). Fundamental differences exist between the mechanisms behind angiogenesis and those behind collateral vessel growth. For example, hypoxia, a major inducer of angiogenesis, is not required for arteriogenesis, which has been shown to rely instead on mechanical forces such as fluid shear stress, which activates the endothelial and SMC wall of the artery and subsequently recruits mononuclear cells essential for the process (reviewed in Heil and Schaper, 2004; Schaper, 2009). Collateral artery growth is indeed generally understood to result from the remodeling of pre-existing arterial connections, not *de novo* artery formation, since sprouting angiogenesis is usually not seen, and hypoxia-inducible genes do not play a role (Deindl et al., 2001). Indeed, it has been shown in models of hindlimb ischemia that angiogenesis and arteriogenesis occur distinctly, and although tissue ischemia and/or VEGF stimulate capillary sprouting and endothelial cell proliferation, the growth and development of larger collateral vessels with subsequent improved collateral flow occurs when VEGF levels are low (Hershey et al., 2001), suggesting that further signals are needed for SMC proliferation.

It is important to note that many of the same mechanisms are involved during arteriogenesis of smaller arteries as in those leading to atherosclerosis in larger vessels, and many pro-arteriogenic factors have been shown to be also pro-atherogenic (van Royen and Schaper, 2004). Among the features seen in both processes are endothelial activation, increased monocyte chemotactic protein-1 (MCP-1) expression and monocyte recruitment, smooth muscle cell proliferation, and matrix-metalloproteinase (MMP) activation. In addition, angiogenesis and vascular growth factors can contribute to atherosclerotic plaque formation (Celletti et al., 2001; Bhardwaj et al., 2005), putting into question the safety of vascular growth factors for therapeutic angiogenesis. However, the significance of this is not altogether clear, and some studies have indicated that vascular endothelial growth factors have no atherogenic effects (reviewed in Khurana et al., 2005; Leppanen et al., 2005).

Arteriogenesis is also dependent on nitric oxide (NO) signaling, which is also stimulated by fluid shear stress. Of the nitric oxide synthases, inducible nitric oxide synthase (iNOS) seems to be the most important for arteriogenesis (Troidl et al., 2010). Interestingly, endothelial nitric oxide synthase (eNOS) seems not to be required for arteriogenesis after distal femoral artery ligation, but rather for angiogenesis and vasodilation (Murohara et al., 1998; Mees et al., 2007). Among other factors involved in arteriogenesis and arterial remodeling, Notch signaling plays an important role in developmental coronary artery maturation, postnatal arteriogenesis and for maintaining vessel integrity (Liu et al., 2003; van den Akker et al., 2008; Cristofaro et al., 2013), involving also the arterial cell surface marker ephrinB2 (Limbouurg et al., 2007; Korff et al., 2008).

As mentioned, the recruitment and activation of mononuclear cells are essential for arteriogenesis (Polverini et al., 1977; Arras et al., 1998). Recently, an important pro-arteriogenic function has been implicated for a special subtype of macrophages, so-called “M2-like” macrophages, as opposed to “M1” macrophages supporting proinflammatory processes (Nucera et al., 2011; Takeda et al., 2011; Hamm et al., 2013).

2. Regulators of myocardial growth, angiogenesis and metabolism

The human heart makes up only about 0.5% of the total body weight but uses 10% of the body's total oxygen consumption and 4% of the total cardiac output (Taegtmeyer, 2007). The heart is a plastic organ, capable of adapting to environmental changes *via* for example myocardial growth or cellular metabolic changes (Hill and Olson, 2008). Cardiac hypertrophy, meaning a thickening of the myocardium, is traditionally divided into physiological *vs.* pathological hypertrophy (reviewed in Dorn, 2007). The latter is usually a result of pressure overload-induced hemodynamic stress and ultimately contributes to heart failure, whereas physiological hypertrophy, most often referring to aerobic exercise-induced cardiac hypertrophy, is by definition a benign and even reversible state. Physiological hypertrophy is seen for example during pregnancy, where the heart adapts to a 40% increase in blood volume and a 45% increase in cardiac output (Hunter and Robson, 1992; Duvekot and Peeters, 1994; Schannwell et al., 2002). However, there is a fine line between physiological and pathological cardiac changes in athletes (Pelliccia et al., 1999; Maron and Pelliccia, 2006), and it has been reported that deconditioning does not always completely reverse exercise-induced cardiac remodeling (Pelliccia et al., 2002). It is also important to note that in athletes, strength training and aerobic conditioning each cause distinct hemodynamic changes (*i.e.* pressure overload *vs.* volume overload) with ultimately different effects on cardiac remodeling (reviewed in Maron and Pelliccia, 2006).

Among the known intracellular signaling pathways involved in cardiac hypertrophy are mitogen-activated protein kinase (MAPK) signaling (Bueno et al., 2000), the phosphoinositide 3-kinase (PI3K)–Akt–mammalian target of rapamycin (mTOR) pathway (Shioi et al., 2000; Condorelli et al., 2002; Shioi et al., 2003; Patrucco et al., 2004), calcineurin–NFAT (nuclear factor of activated T-cells) signaling (Molkentin et al., 1998; Wilkins and Molkentin, 2004), as well as other calcium-dependent kinases such as calmodulin-dependent protein kinases (Passier et al., 2000). At the crossroads, glycogen synthase kinase-3 β (GSK-3 β) plays a modulatory role inhibiting both physiological as well as pathological cardiac growth (Figure 1) (Antos et al., 2002;

reviewed in Kerkela et al., 2007). Interestingly, gene deletion of the cytoplasmic bone marrow kinase in chromosome X (Bmx), a non-receptor tyrosine kinase expressed in arterial endothelium and the endocardium (Ekman et al., 1997; Rajantie et al., 2001) can protect mice from cardiac hypertrophy induced by aortic constriction (Mitchell-Jordan et al., 2008).

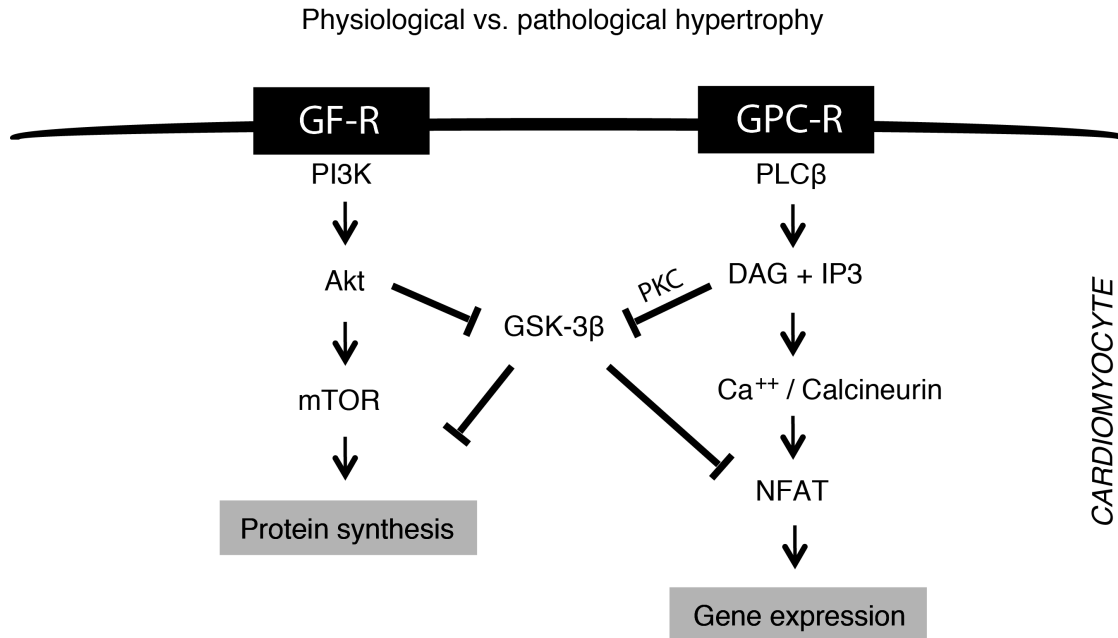


Figure 1. Intracellular signaling pathways associated with physiological (left) vs. pathological (right) cardiac hypertrophy. GF-R, growth factor receptor; PI3K, phosphoinositide 3-kinase; GSK-3β, glycogen synthase kinase-3β; mTOR, mammalian target of rapamycin; GPC-R, G-protein coupled receptor; PLCβ, phospholipase Cβ; PKC, protein kinase C; DAG, diacylglycerol; IP3, inositol triphosphate; NFAT, nuclear factor of activated T-cells. (Adapted from Dorn, 2007; Maillet et al., 2013.)

Prolonged pathological cardiac hypertrophy ultimately leads to decompensation, systolic dysfunction and heart failure (Hill and Olson, 2008). However, synchronized cardiac angiogenesis in animal models of hypertrophy has been shown to be important for preserving cardiac function (Shiojima et al., 2005; Sano et al., 2007). In addition, myocardial hypertrophy can also be induced in mice by angiogenic growth factors alone, where NO signaling seems to play a role (Tirziu et al., 2007; Jaba et al., 2013).

Although the heart relies on mainly fatty acids and glucose as a fuel source, it is capable of burning lactate, ketone bodies and even amino acids (Taegtmeyer, 2007). The heart is very sensitive to changes in blood perfusion, and a reduction in blood flow of only 10-20% can result in exhaustion of the heart's available adenosine triphosphate (ATP) pool. Therefore, flexibility between substrates is crucial in stressed conditions. One important regulator of cardiac metabolism is adenosine monophosphate-activated protein kinase (AMPK), which senses decreases in energy levels and coordinates nutrient uptake and utilization accordingly (reviewed in Zaha and Young, 2012; Maillet et al., 2013).

3. The vascular endothelial growth factor family

The VEGF family consists of five secreted dimeric glycoprotein growth factors in mammals, VEGF (or VEGF-A), VEGF-B, VEGF-C, VEGF-D and PlGF (placenta growth factor). VEGFs belong to the platelet-derived growth factor (PDGF)/VEGF superfamily of growth factors, all containing a VEGF/PDGF homology domain with eight conserved cysteine residues involved in inter- and intramolecular disulfide bond formation. The VEGF ligands are major regulators of blood and lymphatic vessel development and growth and bind with differing specificities to three mainly endothelial transmembrane tyrosine kinase receptors, VEGFR-1/fms-like tyrosine kinase 1 (Flt1), VEGFR-2/human kinase insert domain receptor (KDR)/mouse fetal liver kinase 1 (Flk1) and VEGFR-3/fms-like tyrosine kinase 4 (Flt4). VEGFs also interact with neuropilins (NRP) -1 and -2 (Figure 2A) (reviewed in Pellet-Many et al., 2008).

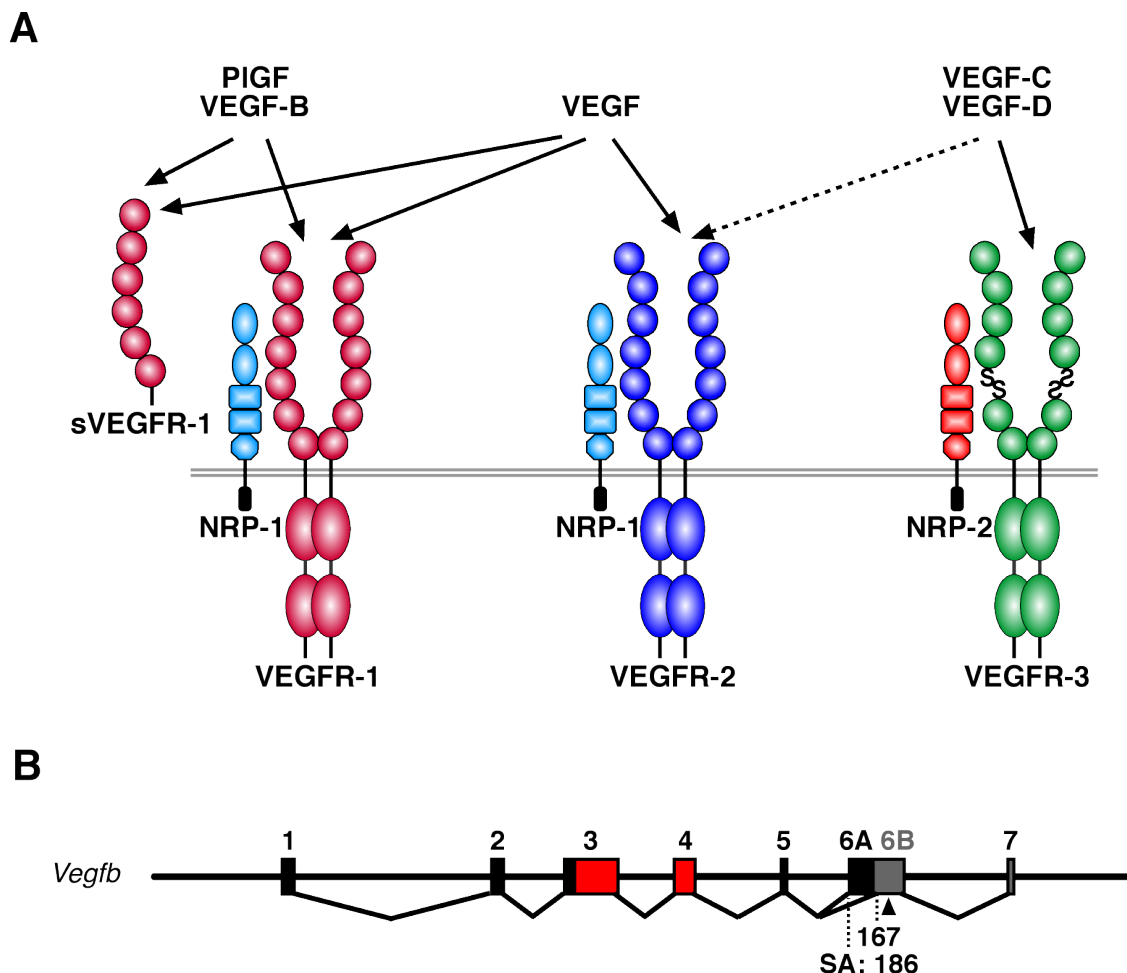


Figure 2. The VEGF family. **A.** Structure and specific binding of VEGFs to their receptors. The dashed line indicates that processing is required before VEGF-C and human VEGF-D can bind to VEGFR-2. (Adapted from Lohela et al., 2009.) **B.** Schematic structure of the *Vegfb* gene. Shown are exons (numbered) and introns with the alternative splice acceptor (SA) sites that produce the VEGF-B₁₆₇ and VEGF-B₁₈₆ isoforms, where exon 6A is lacking from VEGF-B₁₆₇ mRNA. The arrowhead indicates the site of proteolytic processing of VEGF-B₁₈₆. Red, sequence encoding the VEGF homology domain.

3.1. VEGF

VEGF, the archetypal angiogenic growth factor, was first identified as a permeability-inducing factor secreted by tumor cells (Senger et al., 1983) and later as a growth factor for vascular endothelial cells (Ferrara and Henzel, 1989; Leung et al., 1989). VEGF is essential for the development of the vasculature, as mice lacking even a single *Vegfa* allele die at embryonic day (E) 11-12 as a result of impaired angiogenesis and blood island formation (Carmeliet et al., 1996; Ferrara et al., 1996). VEGF binds to receptors VEGFR-1 and VEGFR-2 (De Vries et al., 1992; Quinn et al., 1993), as well as to NRP-1 and NRP-2 (Soker et al., 1998; Gluzman-Poltorak et al., 2000). VEGF exists as several splice isoforms, of which VEGF₁₂₁, VEGF₁₆₅ and VEGF₁₈₉ (in humans) are preferentially expressed (Robinson and Stringer, 2001).

In addition to functioning as a mitogen for ECs, VEGF also regulates EC survival (Alon et al., 1995; Benjamin and Keshet, 1997; Benjamin et al., 1999), mediated through the PI3K–Akt pathway and by inducing the expression of anti-apoptotic proteins (Gerber et al., 1998a; Gerber et al., 1998b). VEGF is also a potent inducer of vascular permeability and inflammation (Gavard and Gutkind, 2006; Nagy et al., 2008). Akt also phosphorylates and activates eNOS, stimulating in turn vasodilation, permeability and angiogenic processes (Fulton et al., 1999; Fukumura et al., 2001; Yu et al., 2005). VEGF also has effects on non-ECs, for example bone marrow derived cells (Clauss et al., 1990; Broxmeyer et al., 1995) and type II pneumocytes (Compernelle et al., 2002).

Overexpression or administration of VEGF results in robust angiogenesis in various tissues (Leung et al., 1989; Isner et al., 1996; Kenyon et al., 1996; Detmar et al., 1998; Larcher et al., 1998; Pettersson et al., 2000), but as mentioned above, it also increases vascular leakage and inflammation (Larcher et al., 1998; Xia et al., 2003), which has hindered its use for therapeutic angiogenesis.

VEGF is upregulated in hypoxia *via* hypoxia inducible factor (HIF)-1 α mediated transcription (Schweiki et al., 1992; Forsythe et al., 1996; Pugh and Ratcliffe, 2003). On the other hand, several growth factors, inflammatory cytokines, oncogenes and hormones have also been reported to induce VEGF (reviewed in Ferrara et al., 2003). Interestingly, nutrient and oxygen deprivation also induce the potent metabolic regulator peroxisome proliferator-activated receptor- γ coactivator-1 α (PGC-1 α), which is able to induce VEGF independently of HIF-1 α in skeletal muscle (Arany et al., 2008), highlighting the close coordination of blood supply and nutrient demand.

3.2. VEGF-B

VEGF-B (previously also known as VRF, VEGF-related factor), first discovered in 1996, has a structure very similar to that of VEGF, and mouse VEGF-B shares approximately 43% amino acid sequence identity with mouse VEGF₁₆₄ (Grimmond et al., 1996; Olofsson et al., 1996a). The gene encoding VEGF-B localizes to chromosome 11q13 in humans, chromosome 19B in mice and chromosome 1q43 in rats (Paavonen et al., 1996; Gerace et al., 2001; Gibbs et al., 2004), and is highly conserved in mammals with about 88% homology at the amino acid level between the mouse and human growth factors (Olofsson et al., 1996a). A primitive form of VEGF-B has also been found in frogs with only 26% homology to human VEGF-B, but

VEGF-B has not been identified in zebrafish (Ruiz de Almodovar et al., 2009). *Vegfb* consists of seven exons and generates two isoforms because of the existence of alternative splice acceptor sites in exon 6 (Figure 2B) (Grimmond et al., 1996; Olofsson et al., 1996b). VEGF-B₁₆₇ has a highly basic heparin-binding carboxy-terminus, whereas VEGF-B₁₈₆ contains a hydrophobic carboxy-terminus and is modified by O-glycosylation and proteolytic processing (Olofsson et al., 1996b). VEGF-B₁₆₇ thus binds tightly to heparan sulfate proteoglycans on the cell surface and in the extracellular matrix, whereas VEGF-B₁₈₆ is freely diffusible. The molecular weights of homodimers of VEGF-B₁₆₇ and VEGF-B₁₈₆ are 42 and 60 kDa, respectively. Both isoforms are simultaneously expressed in various tissues and bind to VEGFR-1 and NRP-1, but not to the major mitogenic endothelial cell receptors VEGFR-2 and VEGFR-3 (Olofsson et al., 1998b; Makinen et al., 1999). Proteolytic processing of VEGF-B₁₈₆ is required for its binding to NRP-1 (Makinen et al., 1999). In culture, VEGF-B is also able to form heterodimers with VEGF (Olofsson et al., 1996a), but this interaction has not been observed *in vivo*.

Unlike VEGF, the expression of VEGF-B does not seem to be directly regulated by hypoxia (Enholm et al., 1997), although hypoxia appeared to induce VEGF-B in the mouse retina in a recent report (Singh et al., 2013). VEGF-B has a wide tissue distribution in mice, being most abundant in tissues with high metabolic activity such as the myocardium, skeletal and vascular smooth muscle, as well as in brown adipose tissue, the brain, kidney, and parietal cells of the stomach (Olofsson et al., 1996a; Lagercrantz et al., 1998; Aase et al., 1999; Capoccia et al., 2009). This could suggest a role for VEGF-B in coordinating the crosstalk between endothelial cell growth and metabolism.

3.2.1. VEGF-B in angiogenesis

Although initial reports indicated that VEGF-B is able to stimulate EC growth *in vitro* (Olofsson et al., 1996a), the ability of VEGF-B to stimulate angiogenesis directly is poor in most tissues. VEGF-B did not stimulate vessel growth when delivered into skeletal muscle or periadventitial tissue with adenoviral vectors (Bhardwaj et al., 2003; Rissanen et al., 2003). VEGF-B also did not improve vascular growth in the ischemic limb (Li et al., 2008a; Lahtenvuo et al., 2009), although some results to the contrary have also been published (Silvestre et al., 2003; Wafai et al., 2009). On the other hand, VEGF-B overexpressed in endothelial cells of transgenic mice was able to potentiate rather than initiate angiogenesis, and unlike VEGF, VEGF-B did not increase vascular permeability (Mould et al., 2005). Overexpression of VEGF-B has similarly been shown to aggravate pathological retinal and choroidal neovascularization in mice (Zhong et al., 2011), and VEGF-B has also been implicated in pathological vascular changes in inflammatory arthritis (Mould et al., 2003). Furthermore, VEGF-B has also been proposed by some to be a survival factor for ECs, regulating the expression of vascular pro-survival genes *via* both NRP-1 and VEGFR-1 (Zhang et al., 2009).

3.2.2. VEGF-B in the heart

Mice deficient of VEGF-B are viable and fertile and display only mild phenotypes in the heart. This is manifested as an atrioventricular conduction abnormality characterized by a prolonged electrocardiographic PQ interval in one strain (Aase et al., 2001), or as a smaller heart size with slightly dysfunctional coronary vasculature

and impaired recovery after myocardial ischemia in another (Bellomo et al., 2000). The latter mouse strain also showed resistance to development of pulmonary hypertension and vascular remodeling during chronic hypoxia (Wanstall et al., 2002). Collectively, the results from models of gene deletion suggest a role for VEGF-B in cardiovascular pathologies.

Interestingly, VEGF-B is expressed in spatial and temporal correlation with the commencement and progression of coronary endothelial growth in the heart, suggesting that it plays a role in coronary vessel development (Bellomo et al., 2000). Importantly, antibodies against VEGF-B were found to inhibit coronary artery development in the quail embryo (Tomanek et al., 2002; Tomanek et al., 2006).

Several studies have indicated a role for VEGF-B in cardiac angiogenesis and/or cardioprotection. VEGF-B levels were found to decrease following experimentally induced myocardial infarction (MI) in rats as well as in heart failure following transverse aortic constriction (Huusko et al., 2012; Zhao et al., 2012). In human patients, low VEGF-B levels were found to accurately predict left ventricular dysfunction and remodeling following MI, suggesting that VEGF-B could be used as a prognostic biomarker with stronger predictive value than troponin T (Devaux et al., 2010; Devaux et al., 2012). Interestingly, the opposite was true for PlGF, as increased PlGF levels predicted heart failure (Devaux et al., 2010).

In experimental models, VEGF-B overexpression has been achieved mainly with adenoviruses or adeno-associated viruses (AAVs). An overdose of VEGF-B₁₈₆ *via* transient adenoviral delivery into the pig myocardium enlarged myocardial vessels after acute infarction, which was inhibited by administration of either soluble VEGFR-1 or soluble NRP-1, but not by blocking VEGFR-2 signaling or NO production (Lahtenvuo et al., 2009). Adenoviral delivery of VEGF-B₁₆₇ enlarged capillaries and ameliorated angiotensin II-induced diastolic dysfunction, with activation of the PI3K–Akt pathway (Serpi et al., 2011). Adenoviral delivery of VEGF-B₁₈₆ was also able to enlarge myocardial capillaries in mice (Huusko et al., 2010). However, AAV-mediated administration of VEGF-B₁₆₇ preserved cardiac contractility and prevented cardiomyocyte apoptosis after experimental myocardial infarction in rats without significant vascular effects (Zentilin et al., 2010). Similar results were achieved in dogs subjected to tachypacing-induced development of dilated cardiomyopathy, where AAV-VEGF-B₁₆₇ administration delayed the progression towards heart failure (Pepe et al., 2010). In addition, a VEGF-B₁₈₆ adenovirus improved systolic function in progressive left ventricular hypertrophy caused by transverse aortic constriction in mice (Huusko et al., 2012). Indeed, the above studies and others (Li et al., 2008a) have implicated the heart as a specific target for VEGF-B induced effects. However, the mechanisms behind these effects are still largely unclear.

3.2.3. Additional roles for VEGF-B

Other studies have implicated a role for VEGF-B in neuroprotection during cerebral ischemia as well as in animal models of neuropathy (Sun et al., 2004; Poesen et al., 2008; Falk et al., 2009), seemingly involving VEGFR-1 expressed in neurons (Li et al., 2008b; Dhondt et al., 2011). VEGF-B expression is also upregulated in some tumor types, such as in ovarian, colorectal, renal cell and prostate cancer (Gunningham et al., 2001; Hanrahan et al., 2003), but its role in tumor progression is poorly

understood. Surprisingly, VEGF-B deficiency in the RIP1-Tag2 mouse model of pancreatic endocrine adenocarcinoma led to increased tumor size, whereas transgenic overexpression of VEGF-B₁₆₇ suppressed tumor growth (Albrecht et al., 2010).

Recent work has investigated a role for VEGF-B in cellular and whole-body metabolism, as VEGF-B is highly expressed in metabolically active tissues. Interestingly, similarly to what was previously published for VEGF (Arany et al., 2008), VEGF-B expression in skeletal muscle is induced by the transcription factor PGC-1 α (Bostrom et al., 2012). In addition, it has been shown that VEGF-B expression and a nuclear-encoded mitochondrial gene cluster set are coordinately regulated (Mootha et al., 2003; Hagberg et al., 2010). On the other hand, the absence of VEGF-B was reported to lead to decreased expression of fatty acid transport proteins (FATPs) in endothelial cells, which correlated with decreased amounts of lipid droplets in cardiomyocytes and skeletal muscle fibers, and accumulation of fat in white adipose tissue (Hagberg et al., 2010). Interestingly, blocking VEGF-B improved insulin sensitivity in mouse and rat models of type II diabetes (Hagberg et al., 2012).

3.3. PlGF

PlGF was originally found in the human placenta shortly after the discovery of VEGF (Maglione et al., 1991) and exists as four isoforms in humans but only one in mice (PlGF-2) (Maglione et al., 1993; Cao et al., 1997; Yang et al., 2003). In addition to the placenta, PlGF is expressed in for example the heart, lungs and skeletal muscle (reviewed in De Falco, 2012). PlGF is very similar to VEGF-B in many respects, but the effects of the two growth factors on angiogenesis and arteriogenesis seem to be considerably different. According to most reports, PlGF binds to the same receptors as VEGF-B, namely VEGFR-1 and NRP-1 (Park et al., 1994; Migdal et al., 1998). PlGF gene-targeted mice are viable, but their angiogenesis and arteriogenesis are impaired in ischemia, inflammation and wound healing, as well as in the hypoxic brain (Carmeliet et al., 2001; Freitas-Andrade et al., 2012). Unlike VEGF-B, PlGF is able to stimulate angiogenesis and collateral growth for example in the ischemic heart and limb with similar efficiency to VEGF (Luttun et al., 2002) and also increases vessel permeability (Odorisio et al., 2002) and inflammation (Oura et al., 2003; Selvaraj et al., 2003). However, in a recent report, intracranial PlGF administration with AAV vectors strongly stimulated angiogenesis and arteriogenesis in the brain without significant inflammation or edema (Gaal et al., 2013). PlGF also stimulates the migration and survival of endothelial cells (Ziche et al., 1997; Adini et al., 2002) and can increase the proliferation of smooth muscle cells (Bellik et al., 2005).

It has been reported in numerous studies that PlGF regulates intermolecular crosstalk between VEGFR-1 and VEGFR-2 and enhancement of VEGF signals *via* VEGF/PlGF heterodimer formation (Park et al., 1994; DiSalvo et al., 1995; Cao et al., 1996; Carmeliet et al., 2001; Autiero et al., 2003). However, PlGF is also capable of inducing unique signals through VEGFR-1 (Landgren et al., 1998; Autiero et al., 2003; Schoenfeld et al., 2004). Some studies have suggested that PlGF mediates its arteriogenic effects *via* recruitment of growth factor-secreting monocytes (Pipp et al., 2003).

Much remains to be learned about the mechanisms of PlGF-induced vascularization. The role of PlGF in tumor angiogenesis is also under considerable controversy

(Fischer et al., 2007; Bais et al., 2010; Yao et al., 2011). Interestingly, in the mouse heart, PlGF is able to induce myocardial angiogenesis and cardiac hypertrophy *via* the Akt-mTORC1 pathway, requiring nitric oxide signaling (Jaba et al., 2013). However, in another report, PlGF was only able to support pressure overload-induced cardiac hypertrophy secondarily through a paracrine mechanism *via* endothelial cells and fibroblasts to induce capillary growth and fibroblast proliferation (Accornero et al., 2011).

3.4. VEGFR-1

VEGFR-1 is composed of an extracellular domain, transmembrane domain, intracellular tyrosine kinase (TK) domain, and carboxy-terminal region (Shibuya et al., 1990). The extracellular domain consists of seven immunoglobulin-like (Ig) domains (Figure 2A), with the ability to bind ligands in the second and third Ig domains (Tanaka et al., 1997). VEGFR-1 binds VEGF, VEGF-B and PlGF with high affinity (De Vries et al., 1992). Mice lacking VEGFR-1 produce an excess of ECs and disorganized vasculature and die *in utero* at E8.5-9, suggesting that VEGFR-1 is mainly a negative regulator of angiogenesis, by preventing binding of VEGF to VEGFR-2 (Fong et al., 1995; Fong et al., 1999). This is consistent with the fact that mice engineered to express a truncated form of VEGFR-1, lacking the TK domain responsible for signaling, are viable (Hiratsuka et al., 1998). Similarly, the deletion of VEGFR-1 in adult mice resulted in endothelial cell proliferation and protected against myocardial infarction at least in part *via* upregulation of VEGFR-2 signaling (Ho et al., 2012).

The tyrosine kinase activity of VEGFR-1 in cultured endothelial cells is weak, and its downstream signaling is poorly understood (Waltenberger et al., 1994; Seetharam et al., 1995; Shibuya, 2006). On the other hand, in addition to ECs, VEGFR-1 is expressed at least on monocytes/macrophages and pericytes, and activation of its TK domain is required for monocyte activation and migration (Barleon et al., 1996; Clauss et al., 1996). VEGFR-1 is also expressed in neurons (Poesen et al., 2008). A soluble form of the VEGFR-1 extracellular domain (sVEGFR-1), which is able to neutralize VEGF (Kendall and Thomas, 1993), has been shown to be involved in the pathogenesis of pre-eclampsia (Levine et al., 2004; Kanasaki et al., 2008). Interestingly, VEGFR-1 is expressed also in the endothelium of coronary vessels in the fetal human heart, whereas VEGFR-2 is not, suggesting that VEGFR-1 could play a role in coronary vessel development (Kaipainen et al., 1993; Partanen et al., 1999). In addition, VEGFR-1 expression is upregulated by hypoxia *via* HIF-1 α binding regulatory sequences, in contrast to VEGFR-2 and VEGFR-3 (Gerber et al., 1997; Zentilin et al., 2010).

The crystal structure of VEGF-B in complex with VEGFR-1 has been described (Iyer et al., 2006; Iyer et al., 2010), revealing structural interaction with domain 2 of VEGFR-1 similarly to that of VEGF and PlGF. VEGF and PlGF also require domain 3 of VEGFR-1 for high-affinity binding (Davis-Smyth et al., 1998; Christinger et al., 2004). However, it was recently shown that VEGF-B differs in its binding to VEGFR-1 in that it does not require binding to domain 3 (Anisimov et al., 2013a). Receptor specificity of VEGF ligands is determined by an amino-terminal α -helix and three peptide loops, and in this study, it was shown that VEGF-B is unable to induce efficient receptor dimerization and signaling downstream of VEGFR-1 as a result of

the unique structure of loop 1 of VEGF-B. Importantly, swapping loop 1 from PlGF to VEGF-B conferred the angiogenic properties of PlGF to the resulting chimera. These results suggest that VEGF-B–VEGFR-1 signaling is in itself weak, and the effects induced by VEGF-B may at least partly occur through inhibiting other ligands from interacting with VEGFR-1, thus inducing more efficient interaction of VEGF with the highly mitogenic VEGFR-2.

3.5. VEGFR-2

VEGFR-2 is the major receptor mediating VEGF-induced angiogenesis by inducing the proliferation, survival, sprouting and migration of ECs, and also by increasing endothelial permeability (Meyer et al., 1999; Gille et al., 2001). VEGFR-2 is structurally similar to VEGFR-1, but although VEGF binds to VEGFR-2 with a lower affinity than to VEGFR-1, the TK activity of VEGFR-2 is much stronger (Waltenberger et al., 1994; Gille et al., 2000). VEGFR-2 is expressed mainly in ECs, and mice lacking VEGFR-2 die at E8.5-9.5 as a result of impaired vasculogenesis and hematopoiesis (Shalaby et al., 1995).

Downstream signaling by VEGFR-2, following binding of VEGF and receptor dimerization and autophosphorylation of several tyrosine kinase residues, involves numerous pathways, including the phospholipase C (PLC)- γ /protein kinase C (PKC) pathway, causing activation of the c-Raf–MEK–MAP kinase cascade (Guo et al., 1995; Xia et al., 1996; Takahashi et al., 1999), as well as of the PI3K–Akt pathway driving cell survival and migration and eNOS activation (see above under VEGF) (Gerber et al., 1998b).

3.6. VEGF-C, VEGF-D and VEGFR-3

VEGFR-3 is the major receptor controlling lymphangiogenesis, or the growth of lymphatic vessels (reviewed in Tammela and Alitalo, 2010). Different forms of VEGF-C and VEGF-D are produced through proteolytic processing, and their affinity for VEGFR-3 increases with processing. The processed mature forms of human VEGF-C and VEGF-D also bind VEGFR-2 (Joukov et al., 1997; Achen et al., 1998), and heterodimer formation between VEGFR-2 and VEGFR-3 has been reported, particularly in the tip cells of angiogenic vessel sprouts (Dixelius et al., 2003; Olsson et al., 2006; Nilsson et al., 2010). Mouse VEGF-D, on the other hand, binds only to VEGFR-3 (Baldwin et al., 2001). VEGFR-3 is present in all endothelia during early stages of development but becomes restricted to mainly lymphatic endothelial cells in the adult (Kaipainen et al., 1995), although expressed in small amounts also in fenestrated blood capillaries (Partanen et al., 2000). VEGFR-3 is, however, highly expressed in angiogenic sprouts and is involved in postnatal retinal and tumor angiogenesis (Laakkonen et al., 2007; Tammela et al., 2008).

Homozygous deletion of *Vegfc* from mouse embryos leads to a complete absence of lymphatic vessels and embryonic lethality as a result of fluid accumulation in tissues; however, the blood vasculature of these mice appears to develop normally (Karkkainen et al., 2004). VEGF-D deficient mice, on the other hand, are healthy and fertile, and display no obvious defects in lymphatic function (Baldwin et al., 2005). Although loss of VEGFR-3 also results in defective blood vessel development and embryonic death by E9.5 (Dumont et al., 1998), the combined deletion of its ligands VEGF-C and

VEGF-D in mice does not cause any additional defects when compared to the loss of VEGF-C alone (Haiko et al., 2008). This may be explained by roles of VEGFR-3 in ligand-independent signaling and VEGFR-2 heterodimerization (Tammela et al., 2011).

Transgenic overexpression of either VEGF-C or VEGF-D in the skin results in hyperplasia of lymphatic vessels (Jeltsch et al., 1997; Veikkola et al., 2001), but the processed forms of the human growth factors also induce blood vascular growth, likely through VEGFR-2 binding (Saaristo et al., 2002; Rissanen et al., 2003; Anisimov et al., 2009).

3.7. Neuropilins

The neuropilins, NRP-1 and NRP-2, were originally identified as receptors for semaphorins, which mediate repulsive signals during neuronal axon guidance (Chen et al., 1997; Kolodkin et al., 1997). NRP-1 and NRP-2 lack cytoplasmic enzyme activity and function as co-receptors, complexing with other transmembrane receptors such as the VEGFRs (reviewed in Pellet-Many et al., 2008). Neuropilins are also expressed as soluble forms of their extracellular domains and released by cells (Gagnon et al., 2000; Rossignol et al., 2000). VEGF isoforms bind with differing specificity to NRP-1 and NRP-2. VEGF₁₆₅ and VEGF₁₂₁ can reportedly interact with NRP-1 (Soker et al., 1998), whereas VEGF₁₆₅ and VEGF₁₄₅ interact with NRP-2 (Gluzman-Poltorak et al., 2000). PlGF-2 and VEGF-B bind only to NRP-1 (Migdal et al., 1998; Makinen et al., 1999), whereas VEGF-C and VEGF-D can interact with both NRP-1 and NRP-2 (Karkkainen et al., 2001; Karpanen et al., 2006). VEGF can mediate complex formation of VEGFR-2 and NRP-1, which was reported to enhance VEGF/VEGFR-2 interactions (Soker et al., 2002). In addition, both NRP-1 and NRP-2 can form complexes with VEGFR-1 (Fuh et al., 2000; Gluzman-Poltorak et al., 2001), and NRP-2 can interact with VEGFR-3 (Karpanen et al., 2006).

NRP-1 is essential for the formation of the vasculature, as mice lacking NRP-1 die at E13.5 as a result of vascular defects (Kawasaki et al., 1999). NRP-2 gene-targeted mice are viable, but show impaired development of small lymphatic vessels and capillaries in addition to neuronal defects (Yuan et al., 2002). However, embryos lacking both NRP-1 and NRP-2 have an aggravated blood vascular phenotype and die *in utero* at E8.5, implicating compensatory mechanisms between the neuropilins (Takashima et al., 2002). In the heart, NRP-1 is expressed similarly to VEGFR-1 in coronary vessels, myocardial capillaries as well as epicardial vessels (Partanen et al., 1999). Interestingly, NRP-1 is also expressed in the developing myocardium and endocardium in mouse embryos at E12.5 (Makinen et al., 1999).

AIMS OF THE STUDY

This study was undertaken in order to elucidate the role of VEGF-B in the heart as well as its therapeutic potential, focusing on its effects on cardiomyocytes and cardiac blood vessels.

The specific aims were:

- I To study and compare the effects of overexpression of VEGF-B in the mouse skin and heart, particularly effects of VEGF-B on blood vasculature, lipid metabolism, and heart function.
- II To investigate the mechanisms behind VEGF-B action in the heart and improve our understanding of the effects of VEGF-B on cardiovascular physiology with a novel rat model.
- III To study the therapeutic potential of VEGF-B-induced vessel growth in the rat heart and examine the effects of VEGF-B loss-of-function in the rat, as well as the downstream signaling pathways involved.

MATERIALS AND METHODS

The materials and methods used in this study are described in detail in the original publications. A summary of the most relevant materials and methods is provided below.

Table. Materials

| Mouse line | Description | Used in | Source/reference |
|------------------------------|--|---------|--------------------------|
| <i>Bmx</i> ^{-/-} | <i>Bmx</i> gene deletion | II | (Rajantie et al., 2001) |
| C57Bl/6J | Wildtype inbred mice | II, III | Charles River Inc. |
| FVB/N | Wildtype inbred mice | II | Harlan Inc. |
| K14-VEGF-B | Overexpresses human VEGF-B in basal epidermal keratinocytes | I | I |
| <i>Vegfb</i> ^{-/-} | <i>Vegfb</i> gene deletion | III | (Bellomo et al., 2000) |
| VEGFR-1 TK ^{-/-} | Lacks the tyrosine kinase domain of VEGFR-1 | II | (Hiratsuka et al., 1998) |
| αMHC-VEGF-B | Overexpresses both isoforms of human VEGF-B in cardiomyocytes | II | II |
| αMHC-VEGF-B ₁₆₇ | Overexpresses human VEGF-B ₁₆₇ in cardiomyocytes | I | I |
| αMHC-VEGF-B _{Ex1-5} | Overexpresses the first five exons of mouse VEGF-B in cardiomyocytes | II | II |
| Rat line | Description | Used in | Source/reference |
| <i>Vegfb</i> ^{-/-} | <i>Vegfb</i> gene deletion | III | III |
| Wistar (HsdBr1:WH) | Wildtype outbred rats | II, III | Harlan Inc. |
| αMHC-VEGF-B | Overexpresses both isoforms of human VEGF-B in cardiomyocytes | II, III | II |
| Recombinant virus | Description | Used in | Source/reference |
| AAV-HSA | Adeno-associated virus that encodes human serum albumin | II, III | II |
| AAV-PIGF | Adeno-associated virus that encodes mouse PIGF | II | II |
| AAV-VEGF | Adeno-associated virus that encodes mouse VEGF ₁₂₀ | II | II |
| AAV-VEGF-B ₁₆₇ | Adeno-associated virus that encodes mouse or human VEGF-B ₁₆₇ | II, III | II |
| AAV-VEGF-B ₁₈₆ | Adeno-associated virus that encodes mouse or human VEGF-B ₁₈₆ | II, III | II |
| Antigen | Antibody | Used in | Source/reference |
| CD45 (rat) | Mouse monoclonal | II, III | BD Biosciences |
| CD45 (mouse) | Rat monoclonal | III | BD Biosciences |
| Collagen IV (mouse) | Rabbit | I | Cosmo Bio |
| Dystrophin (human) | Mouse monoclonal (clone Dy8/6C5) | II, III | Novocastra |
| ED-1/CD68 (rat) | Mouse monoclonal (MCA341R) | II, III | AbD Serotec |
| F4/80 (mouse) | Rat monoclonal | II | AbD Serotec |
| Laminin-1 | Rabbit anti-serum | I | Päivi Liesi |
| Neuropilin-1 (rat) | Goat polyclonal (AF566) | I | R&D Systems |
| PAI-1 (mouse) | Rabbit | II | Peter Andreasen |
| PECAM-1 (mouse) | Rat monoclonal (clone MEC13.3) | I, II | BD Biosciences |
| SMA (human) | Mouse monoclonal-Cy3 (clone 1A4) | II, III | Sigma |
| VEGF-B (human) | Goat polyclonal (AF751) | I, II | R&D Systems |
| RECA-1 (rat) | Mouse monoclonal (MCA970) | II, III | AbD Serotec |
| VEGFR-1 (mouse) | Rat monoclonal (5B12) | I, III | ImClone Systems |

Animal models (I, II, III)

All experiments involving mice or rats were approved by the Provincial State Office of Southern Finland and carried out in accordance with institutional guidelines. Transgenic VEGF-B mouse models were generated by injection of expression cassettes into fertilized mouse oocytes of FVB/N background. To generate the K14-VEGF-B transgenic mice (I), DNA from the human VEGF-B gene corresponding to nucleotides 745-5059 of Genbank accession number AF468110 was cloned into the keratin-14 expression vector (kindly provided by Dr. Elaine Fuchs) (Vassar et al., 1989), and one noninitiating upstream ATG was mutated into a GTG. To generate the heart-specific VEGF-B₁₆₇ transgene (I), the recessed 3'-ends of the EcoRI fragment from a human VEGF-B₁₆₇/pCRII vector (Olofsson et al., 1996a) were filled in with the Klenow fragment of DNA polymerase I and ligated to the Sall-opened and Klenow filled-in α -myosin heavy chain (α MHC) promoter expression vector (a kind gift from Dr. Jeffrey Robbins).

For generation of mice and rats overexpressing both isoforms of human VEGF-B in cardiomyocytes (II, III), a fragment of the human VEGF-B gene was isolated from the K14-VEGF-B construct (I) and cloned into the α MHC promoter expression vector. To generate α MHC-mVEGF-Bex1-5 mice (II), the mVEGF-Bex1-5 fragment (encoding VEGF-B with the following carboxy-terminal amino acid residues: VKPD) was isolated from the mVEGF-Bex1-5-pSubCMV-WPRE vector with MluI, blunted and cloned into the α MHC promoter expression vector. Transgenic animals were generated by microinjection of fertilized oocytes from FVB/N mice or outbred HsdBrl:WH Wistar rats.

VEGF-B gene-deleted rats of Sprague-Dawley background (III) were generated using a zinc-finger nuclease based technique by Sigma Advanced Genetic Engineering Labs, Sigma-Aldrich Biotechnology (St. Louis, Missouri, USA) (Cui et al., 2011). A 22-base pair segment of exon 1 of the rat VEGF-B gene was replaced with a bacterial *lacZ* gene with a nuclear localization signal (kindly provided by Dr. Thomas Quertermous) (Sheikh et al., 2008) following the endogenous Kozak sequence. Wildtype Sprague-Dawley littermates were used as controls.

Histochemistry and immunohistochemistry (I, II, III)

Tissue samples were either frozen in Optimal Cutting Temperature compound for cryosectioning or embedded in paraffin following fixation and dehydration. Paraffin sections were prepared for stainings *via* deparaffination, rehydration and antigen retrieval. For histochemistry, sections were stained with hematoxylin-eosin, resorcin-fuchsin, Herovici's stain for collagen, or Masson's trichrome. For immunostaining of frozen sections, sections were fixed with cold acetone, washed, and blocked in TNB (PerkinElmer) or 5% donkey serum with 0.2% bovine serum albumin. For whole-mount staining of mouse ears or staining of thick 200 μ m heart sections, samples were fixed with 4% paraformaldehyde. The primary antibodies used are detailed in the Table. For immunofluorescence, Alexa Fluor 488, 594 and 647-conjugated secondary antibodies (Molecular Probes) were used for detection, and samples were mounted with Vectashield mounting medium containing 4,6-diamidino-2-phenylindole for nuclear staining (Vector Laboratories). For light microscopy, biotinylated secondary antibodies (Vector Laboratories) were used followed by detection using the Tyramide

Signal Amplification kit (NEN Life Sciences/PerkinElmer), 3-amino-9-ethylcarbazole substrate (Sigma-Aldrich), and hematoxylin counterstaining.

Fluorescently labeled samples were imaged using an Axioplan2 fluorescence microscope (Zeiss) or a confocal LSM 510 Meta or LSM 5 Duo microscope (Zeiss). Peroxidase-stained samples were imaged with a Leica DM LB research microscope. Image analyses were carried out using the ImageJ software (National Institutes of Health) from several randomly chosen photographic fields from each sample.

Western blotting (I, II, III)

Tissue samples were sliced into small pieces, mixed with RIPA lysis buffer (150 mM NaCl, 1% NP-40, 0.5% deoxycholic acid, 0.1% sodium dodecyl sulfate, 50 mM Tris pH 8.0, 20 µg/mL leupeptin, 3.4 µg/mL aprotinin, 1 mM Na₃VO₄, 1 mM PMSF) in Lysing Matrix tubes (MP Biomedicals), and homogenized. Total protein concentrations were measured using the BCA Protein Assay Kit (Thermo Scientific). Lysates were boiled in Laemmli sample buffer (LSB), and equal amounts of total protein samples were subsequently separated in SDS-PAGE, transferred onto a nitrocellulose membrane and incubated with primary antibodies, followed by a horseradish peroxidase-conjugated secondary antibody. Antibody complexes were visualized on X-ray film using chemiluminescent substrate (Thermo Scientific).

Transmission electron microscopy (I, II, III)

Tissue samples were fixed in 2.5% glutaraldehyde, postfixed and embedded in epon. Semithin sections were stained with toluidine blue, and on the basis of initial analysis in light microscopy, regions of interest were selected for thin (100 nm) sectioning and analysis using a JEOL 1400 EX or Philips EM-400 Transmission Electron Microscope.

Blood pressure analysis (I, II)

Heart rate and mean arterial pressure were recorded from the left carotid artery in mice using telemetric implants (Butz and Davisson, 2001) (I). Blood pressure was measured in rats with the CODA Non-Invasive Blood Pressure System for Mice and Rats (Kent Scientific Corporation) on non-anesthetized animals restrained in a rodent holder (II).

Echocardiography (I, II, II)

Transthoracic echocardiography was performed on anesthetized animals with an Acuson Sequoia 512 Ultrasound System and an Acuson Linear 15L8 transducer (Siemens). Normal body temperature was maintained.

Measurements in isolated, perfused hearts (I)

The mouse aorta was cannulated after cervical dislocation and perfusion commenced immediately. The heart was then excised and perfusion continued *ex vivo*. Left ventricular pressure was monitored using a saline-filled cannula connected to a Statham P231D pressure transducer and SP1400 pressure monitor. Venous effluent

from the heart was collected in one-minute aliquots, and the lactate dehydrogenase washout was measured.

Recombinant AAV vector preparation (II, III)

cDNAs were cloned into blunted MluI and NheI restriction sites of the psubCMV-WPRE recombinant AAV expression vector. The recombinant AAVs (serotype 9) were produced as described previously (Anisimov et al., 2009).

Micro-CT imaging of the cardiac vessels (II, III)

Post mortem coronary angiographies were first performed (II) using the Inveon micro-computed tomography (CT) scanner (Siemens). The ascending aorta was cannulated, clamped and filled with 0.3 mL of iodinated intravascular contrast agent eXIATM160XL (Binitio Biomedical Inc.). The coronary arterial and venous trees were segmented using the ADW 4.4 Workstation (General Electric) and visualized as three-dimensional volume rendered images.

High-resolution micro-CT imaging (III) was performed according to Tirziu *et al.* (Tirziu et al., 2005). The aorta was cannulated retrogradely proximal to the brachiocephalic trunk, and the hearts were perfused with heparin (100 IU/kg) followed by adenosine (1 mg/ml) and then perfusion-fixed with 4% paraformaldehyde. The coronary arterial tree was filled with contrast agent consisting of 20% bismuth oxychloride (Sigma-Aldrich) in 5% gelatin, filling only the arterial vessels. Filled hearts were imaged with a high-resolution micro-CT imaging system (GE eXplore Locus SP) followed by morphometric analysis of the arterial vessels.

Experimental myocardial infarction (III)

Myocardial infarction was induced in rats by ligation of the left coronary artery (LCA). Infarct sizes were estimated from Masson's trichrome stained transverse heart sections (Pfeffer et al., 1979).

Positron emission tomography (PET) (II, III)

Rats were given a slow bolus of ^{11}C -acetate (0.4–1.0 ml) and imaged using the Inveon microPET scanner (Siemens). Myocardial blood flow, oxygen consumption and efficiency were estimated from the images. For validation of infarct size measurements (III), a subgroup of the rats was injected in a separate imaging session with ^{18}F -fluorodeoxyglucose, a marker of myocardial glucose metabolism and viability.

Quantitative reverse transcription PCR (III)

Total RNA was isolated from the left ventricle with the TRIsure reagent (Bioline) and further purified with NucleoSpin RNA II (Macherey-Nagel). RNA was transcribed to cDNA using the iScript kit (Bio-Rad), and quantitative PCR was carried out following standard procedures with the SYBR green or TaqMan primer-probe sets. All data were normalized to 18S, β -actin and TBP (TATA-binding protein) housekeeping genes, and quantification was performed using the $2^{-\Delta\Delta\text{CT}}$ method.

Microarray analysis (III)

RNA samples were analyzed with the genome-wide Illumina RatRef-12 Expression BeadChip (BD-27-303; Illumina Inc.) or Affymetrix Rat Gene 2.0 chips. Illumina's GenomeStudio software was used for initial data analysis and quality control. Detailed data analyses were performed with the Chipster software (<http://www.chipster.csc.fi>). After quantile normalization, statistically significant differences in individual genes between the groups were tested using Empirical Bayes statistics and the Benjamin-Hochberg algorithm controlling false discovery rate (FDR). Adjusted FDR values of $P < 0.05$ were considered significant.

Lipidomics (I) and metabolomics (III)

For lipidomics (I), lipid extracts were analyzed on a Waters Q-ToF Premier Mass Spectrometer (Waters, Inc.) combined with an Acquity UltraPerformance Liquid Chromatograph. For metabolomics (III), samples were extracted and prepared for analysis using Metabolon's standard solvent extraction method (Metabolon Inc.). The extracted samples were split into equal parts for analysis on the gas chromatography–mass spectrometry and liquid chromatography–tandem mass spectrometry platforms. Detection and quantification of malonyl-coenzyme A esters (III) was accomplished by extracting coenzyme A esters from powdered tissue and measuring with a modified high-performance liquid chromatograph.

Statistical analysis (I, II, III)

Values were presented as means \pm SD or SEM. Statistical analysis was performed with one-way ANOVA (with Tukey's post-hoc test), the two-tailed unpaired Student's t-test or the Mann-Whitney U test, where appropriate. Differences were considered statistically significant at $P < 0.05$.

RESULTS AND DISCUSSION

The main results of the study are summarized and discussed here. A detailed discussion can be found in the original publications.

1. A novel role for VEGF-B in cardiac hypertrophy and lipid metabolism (I)

Although VEGF-B is closely related to other members of the VEGF family, its effects on blood vessel growth have been shown to be extremely modest. However, VEGF-B is highly expressed in tissues with active energy metabolism, such as the myocardium, skeletal and vascular smooth muscle, as well as in brown adipose tissue (Olofsson et al., 1996a; Aase et al., 1999). We endeavored to elucidate the possible role of VEGF-B in the heart using transgenic mice expressing heparin-binding human VEGF-B₁₆₇, which has been published to be the most abundant isoform (Li et al., 2001), under the myocardium-specific α -myosin heavy chain (α MHC) promoter. At the same time, we compared the effect of overexpression of VEGF-B in the skin, using the keratin-14 promoter expressed in basal keratinocytes in the epidermis (Vassar et al., 1989).

Similarly to previously published results for other tissues (*e.g.* Rissanen et al., 2003), VEGF-B did not cause robust angiogenesis in the heart or skin in mice. However, the hearts overexpressing VEGF-B₁₆₇ were larger and heavier than their littermate controls, as calculated from heart-to-body weight ratios. The hypertrophy was associated with an increase in the cross-sectional diameter of the cardiomyocytes, and in transthoracic echocardiography, the VEGF-B overexpressing hearts showed concentric cardiac hypertrophy, with thicker wall dimensions but no change in diastolic left ventricular diameter. Surprisingly, the VEGF-B transgenic mice had lower blood pressure and heart rate, indicating that the cardiac hypertrophy did not result from pressure overload, but that it was due to intrinsic changes in the myocardium.

Although VEGF-B overexpression actually led to a decrease in capillary density as a result of the increased size of cardiomyocytes, the capillaries in VEGF-B transgenic hearts were larger, with an increase in the number of endothelial cells per vessel cross-section. This indicated a mild proliferation of endothelial cells, which however did not lead to an increase in capillary sprouts. Thus the effect of VEGF-B on blood vessels differed from *e.g.* the effects of VEGF.

Echocardiography revealed that the hypertrophy induced by VEGF-B did not cause significant changes in the systolic function of the heart even at twelve months of age. In addition, the VEGF-B transgenic hearts responded similarly to treatment with angiotensin II, indicating that their tolerance of pressure overload was not compromised despite the hypertrophy. Also, no obvious differences in mitochondrial energy coupling or the basal metabolic rate could be seen, and isolated transgenic hearts showed less damage following ischemia-reperfusion, as seen by an initial decrease in the washout of lactate dehydrogenase.

On the other hand, we observed decreased survival of the VEGF-B transgenic mice by six months of age, likely as a result of a propensity toward arrhythmias. Vacuoles could be seen inside cardiomyocytes of the VEGF-B overexpressing hearts in light microscopy at one year of age, seemingly resulting from damaged mitochondria seen

in electron microscopy at earlier time points, although mitochondrial function appeared normal. Associated with these pathological changes was an increase in *de novo* ceramide synthesis, likely a reason for the lysis/autophagy of mitochondria. Interestingly, we also observed a decrease in the amount of triacylglycerols in the VEGF-B transgenic hearts. VEGF-B thus seemed to have a novel function in lipid metabolism, but whether these metabolic effects were a cause or consequence of the hypertrophy induced by VEGF-B could not yet be concluded from this study.

2. VEGF-B as a novel growth factor for coronary arteries (II)

As the signals mediating the effects of VEGF-B in the heart were still unknown, we proceeded with additional animal models to analyze the mechanisms behind the hypertrophy induced by VEGF-B and simultaneously searched for other actions of VEGF-B. We proceeded first to compare the effects of VEGF-B and other members of the VEGF family on blood vessels in mouse skeletal muscle using local injection of recombinant AAV vectors. VEGF-B did not induce blood vessel growth in skeletal muscle during four weeks of expression, but importantly, it also did not increase inflammation or vessel permeability like VEGF or PlGF. Thus, if VEGF-B could be used therapeutically for example in the heart, as has also been suggested by other groups (Li et al., 2008a; Lahteenvuo et al., 2009; Zentilin et al., 2010), toxicity as a result of vascular leakage should not be a major problem.

As rats are better suited for studies of cardiovascular physiology, we proceeded to create a transgenic rat model, this time using the full-length human VEGF-B gene, producing both VEGF-B₁₆₇ and VEGF-B₁₈₆ under the α MHC-promoter. Similarly to what we previously observed for mice, VEGF-B was able to induce cardiac hypertrophy associated with decreased blood pressure and heart rate, as well as capillary enlargement. In contrast to the mouse model however, we could not observe degenerative changes in the rat cardiomyocytes overexpressing VEGF-B. This seemed to be a result of a robust expansion of the coronary arterial tree, including branches extending into the subendocardial region (Figure 3). Coordinated blood vessel growth has indeed been shown to be important for maintaining heart function in cardiac hypertrophy (Shiojima et al., 2005; Sano et al., 2007). Importantly, the subendocardium is the first area to suffer from ischemia as a result of hypertension, coronary artery disease, or aging (Lumens et al., 2006), and the subendocardial coronary arterial plexus has previously been shown to be an important reserve in coronary artery disease (Hoffman and Buckberg, 1975). Although others have shown that strong overexpression of VEGF-B can increase arterial growth following myocardial ischemia (Lahteenvuo et al., 2009), our study was the first to demonstrate that VEGF-B can induce arteriogenesis without any initial ischemic insult. The coronary arteriogenesis was associated with increased expression of plasminogen activator inhibitor (PAI)-1 in arterial smooth muscle. PAI-1 plays an important role in the regulation of matrix degradation during angiogenesis (Pepper, 2001) as well as in myoendothelial junction formation (Heberlein et al., 2010), and VEGF-B has also previously been shown to activate PAI-1 in endothelial cells in culture, similarly to VEGF (Pepper et al., 1991; Olofsson et al., 1998a).

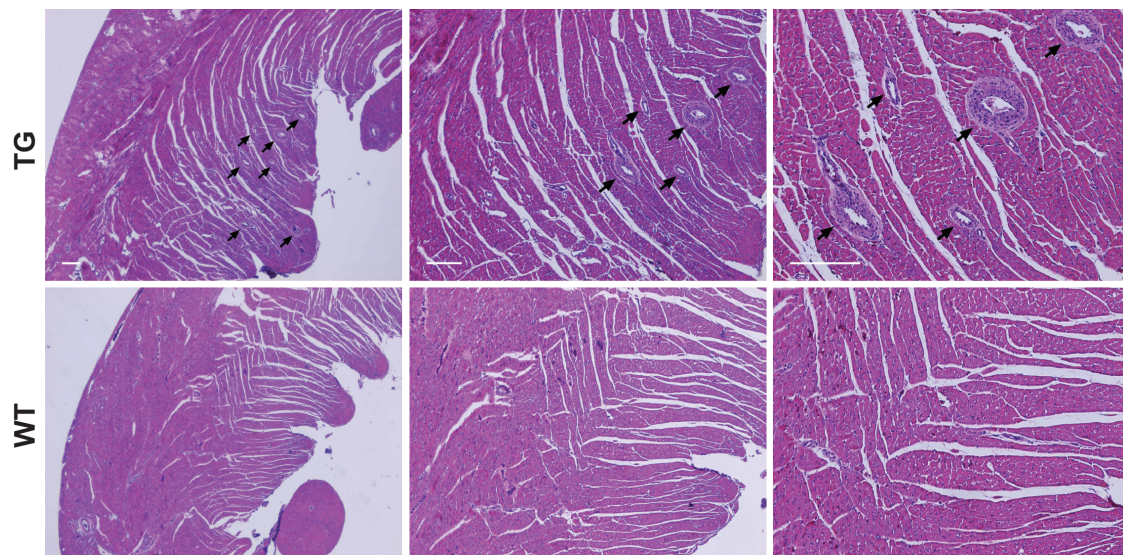


Figure 3. Subendocardial arteriogenesis in VEGF-B transgenic (TG) rat hearts. Representative images of transverse left ventricular sections from transgenic (TG) and wildtype (WT) rats stained with hematoxylin-eosin. Arrows indicate large subendocardial arteries. Scale bars: 200 μ m.

Since VEGF-B binds to two receptors, VEGFR-1 and NRP-1 (Olofsson et al., 1998b; Makinen et al., 1999), we next endeavored to elucidate which of these is required for the effects of VEGF-B in the heart using genetic mouse models. We overexpressed a truncated form of VEGF-B containing only the first five exons, with the ability to bind to VEGFR-1 but not to NRP-1 (Makinen et al., 1999). This form of VEGF-B was still able to induce cardiac hypertrophy, indicating that NRP-1 is not required for this effect of VEGF-B. However, the VEGF-B transgene was not able to increase heart size in mice lacking the tyrosine kinase domain of VEGFR-1 (Hiratsuka et al., 1998), indicating that VEGFR-1 signaling is important for the VEGF-B induced cardiac hypertrophy. We proceeded to investigate a possible role for Bmx, a non-receptor tyrosine kinase expressed mainly in the endothelium of large arteries, since VEGFR-1 was previously shown to increase Bmx phosphorylation and TK activity *in vitro* (Rajantie et al., 2001). In addition, Bmx has been implicated by others to be required for pressure overload induced cardiac hypertrophy (Mitchell-Jordan et al., 2008). Crossing the VEGF-B transgenic mice with Bmx deficient mice indeed significantly attenuated the hypertrophy induced by VEGF-B, suggesting that signaling *via* Bmx and the arterial endothelium is involved in the induction of hypertrophy by VEGF-B. Since Bmx and VEGFR-1 are expressed primarily in endothelial cells in the heart (Partanen et al., 1999), additional unknown signals from endothelial cells would be required for effects of VEGF-B on cardiomyocytes.

3. VEGF-B protects the heart from myocardial ischemia and alters cardiac energy metabolism (III)

As the vast coronary arteriogenesis in VEGF-B transgenic rat hearts showed considerable therapeutic promise for this growth factor in the heart, we next endeavored to characterize the phenotype of the rats more closely and test their performance in stressed conditions. We also strove to elucidate the metabolic role of

VEGF-B in the heart, since results from other groups have implicated a role for VEGF-B in endothelial fatty acid uptake (Hagberg et al., 2010; Hagberg et al., 2012), and since our results from mice also indicated some role for VEGF-B in cardiac energy metabolism (I).

High-resolution micro-CT imaging of the heart revealed an expansion of coronary arteries of all sizes in VEGF-B transgenic rats, but mainly in the largest arteries. Importantly for possible therapeutic applications, we were able to reproduce most of this phenotype using recombinant AAV-VEGF-B administered systemically to adult rats. Interestingly, most previous studies describing effects of VEGF-B on blood vessels in the heart have used very robust but transient overexpression *via* adenoviral delivery (Lahtenvuo et al., 2009), whereas we can achieve clear effects with expression levels closer to physiological levels of VEGF-B (about 6-8 fold over endogenous levels).

To test whether the expanded collateral arteries were functional in VEGF-B transgenic hearts, we subjected the rats to myocardial infarction induced by ligation of the left coronary artery. The resulting infarcts were indeed significantly smaller in the VEGF-B transgenic hearts, which showed improved blood perfusion and cardiac function when compared to wildtype hearts. Importantly, the VEGF-B transgenic hearts maintained their systolic function and during aging actually showed increased stroke volume when compared to wildtype hearts, confirming the physiological nature of the cardiac hypertrophy in VEGF-B transgenic rats.

Since we had shown that VEGFR-1 signaling is involved in the induction of hypertrophy by VEGF-B (II), we next undertook to find the mechanisms behind the growth of cardiac vessels. Increased phosphorylation of VEGFR-2 and its downstream targets were observed following intravenous administration of VEGF protein to VEGF-B overexpressing animals, indicating that VEGF-B, while occupying VEGFR-1, is able to increase VEGF-VEGFR-2 signaling. This effect would however not be as robust as the angiogenesis caused by VEGF overexpression, since it would regulate signaling at endogenous, physiological VEGF levels. Blocking VEGFR-2 signaling did indeed reduce the vessel enlargement seen in VEGF-B overexpressing mice. Similarly, in VEGFR-1 deficient mice, upregulation of VEGFR-2 has been shown to contribute to increased angiogenesis and protection against ischemic damage (Ho et al., 2012).

We next generated a rat model of VEGF-B gene deletion, and similarly to what has previously been published for mice (Bellomo et al., 2000; Aase et al., 2001), loss of VEGF-B did not have obvious effects on blood vessel development. When the VEGF-B deficient rats were subjected to myocardial infarction, no significant differences in cardiac function could be observed; however, the histologically quantified infarct areas were larger in VEGF-B deficient hearts. Some compensatory mechanisms are thus present in the context of constitutive VEGF-B gene deletion, but loss of VEGF-B does seem to mildly impair the coronary vasculature in stressed conditions, as has been published for isolated VEGF-B knockout mouse hearts subjected to ischemia (Bellomo et al., 2000).

Importantly, we were not able to observe any differences in fatty acid uptake or triglyceride content between the VEGF-B wildtype, transgenic or gene-deleted rat

hearts, challenging an existing theory that VEGF-B regulates endothelial fatty acid uptake (Hagberg et al., 2010; Hagberg et al., 2012). Thus it is clear that the metabolic effects proposed for VEGF-B are not as simple as has been suggested.

In our rat models of VEGF-B overexpression, we could however observe a shift from fatty acid to glucose usage in the heart, while pathways directing lipid/macromolecular synthesis, supportive of cell and vessel growth, were induced. Although a shift towards glycolysis occurs in pathological hypertrophy, in our models this was not accompanied by an increase in genes associated with pathological hypertrophy, and blood supply and nutrient usage remained efficient in our models. The failing heart is indeed characterized by an inefficiency to use either substrate group efficiently, and efficient glucose usage has been suggested to slow the progression of heart failure (Taegtmeyer, 2002). In fact, activation of fatty acid metabolism actually results in contractile failure in the hypertrophied rat heart (Young et al., 2001), and drugs favoring glucose oxidation can protect the ischemic heart (Kantor et al., 2000; Abozguia et al., 2010). In summary, close regulation of metabolic pathways seems to be essential for maintenance of heart function. The various effects of VEGF-B in the rat heart are summarized below (Figure 4).

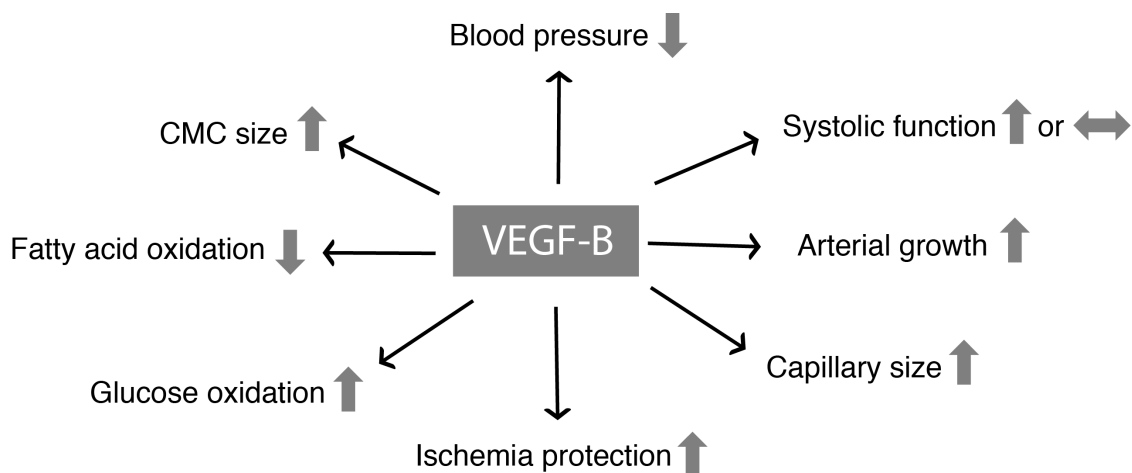


Figure 4. Summary of the effects of VEGF-B in the rat heart. Gray arrows indicate an increase, decrease, or no change. CMC, cardiomyocyte.

CONCLUDING REMARKS

New therapeutic strategies are needed for the treatment of ischemic heart disease, and research on growth factors regulating vascular growth in the heart has recently been fruitful. However, most angiogenic growth factors also increase inflammation and vessel permeability (Lee et al., 2000); thus there are obstacles on the road towards efficient and safe gene therapy for ischemic diseases.

Among VEGFs, PlGF has shown promise in animal models of myocardial ischemia, enhancing regional blood flow and preserving contractile function (Kolakowski et al., 2006; Liu et al., 2013), at least in part through upregulation of VEGF (Lahtenvuo et al., 2009). It is of interest that PlGF seems mainly to increase the growth of capillaries and smaller arterioles in the myocardium (Jaba et al., 2013), whereas in our models, the effects of VEGF-B were strongest in larger arterioles and arteries (III). In addition, adenoviral administration of VEGF-C has been shown to increase collateral vessel formation in a model of myocardial ischemia in pigs (Patila et al., 2006). Adenoviral delivery of VEGF or the mature form of VEGF-D was also able to increase angiogenesis at least in the non-ischemic myocardium; however, increased vessel permeability became an issue at higher doses (Rutanen et al., 2004; Lahtenvuo et al., 2009). So far, in phase II/III clinical trials, intracoronary or intramyocardial VEGF administration has only resulted in limited or no benefit in patients with severe coronary artery disease (reviewed in Yla-Herttuala et al., 2007; Yla-Herttuala, 2013). However, additional trials are ongoing, and it is possible that patients with earlier stage disease would respond better to angiogenic gene therapy, and delivery methods for achieving sufficient growth factor concentrations in the human heart also need to be improved. There is also the possibility of using chimeric growth factors in order to achieve optimal efficiency with fewer side effects (Anisimov et al., 2013b).

Both our results as well as results from other groups have presented VEGF-B as a promising therapeutic vector in experimental models of myocardial ischemia and/or heart failure. In our hands, VEGF-B induces cardiac hypertrophy as well as enlarges coronary arteries and myocardial capillaries in the rat heart. Importantly, VEGF-B does not induce inflammation or vascular leakage. Instead, the effects of VEGF-B on cardiac blood vessels seem to be caused by fine regulation of VEGF–VEGFR-2 signaling by VEGF-B, while the cardiac hypertrophy seems to involve VEGFR-1–Bmx signaling.

Importantly, the hypertrophied VEGF-B transgenic rat hearts maintained improved systolic function also during aging, and they were protected from ischemic damage caused by coronary artery ligation. In mouse hearts, pathological changes could be seen inside cardiomyocytes while the effects on blood vessel growth were milder, suggesting differences in collateral artery formation between the species.

VEGF-B signaling, however, does remain enigmatic. Since its receptors are mainly expressed on blood vascular endothelial cells, additional signals from endothelial cells would be needed for effects on cell growth and metabolism of the cardiomyocytes themselves. It is also conceivable that VEGFR-1 in inflammatory cells could play a role, or additional unknown receptors.

Finally, administration of VEGF-B with AAV-VEGF-B seemed to be efficient and safe. However, the effects of VEGF-B overexpression required two to three weeks of expression before becoming apparent, so it is perhaps not conceivable that future therapies based on VEGF-B would be helpful in acute myocardial infarction, but rather could be beneficial during long-term recovery and in strengthening the myocardium by inducing favorable metabolic changes in cases of ischemic heart disease. The close interplay between angiogenesis and oxidative metabolism will likely be the focus of numerous studies in the near future, and VEGF-B is one potential candidate molecule in this crosstalk.

ACKNOWLEDGEMENTS

These studies were carried out during the years 2007-2013 in the Translational Cancer Biology Laboratory (former Molecular/Cancer Biology Laboratory) in the excellent research facilities of the Research Programs Unit, Biomedicum Helsinki and the Haartman Institute.

I am deeply grateful to my supervisor Kari Alitalo for the opportunity to work in his exceptional research group of outstanding scientists and high-quality laboratory facilities. I am especially thankful to Kari for his commitment to his students and to science and for the excellent scientific training I have received.

I am indebted to Heikki Ruskoaho and Risto Kerkelä for their thorough review of my thesis and for their valuable comments. I am also grateful to the Helsinki Biomedical Graduate Program and its faculty for the funding and opportunities provided by the graduate school. My collaborators, especially Leif Andersson, Eero Mervaala, Juhani Knuuti, Leena Alhonen, Karl Lemström and Seppo Ylä-Herttuala, are thanked for their significant contributions to these studies.

All present and past members of the Alitalo lab and neighboring labs are acknowledged for their support and companionship over the years both in and outside of the lab. I am sincerely thankful to Riikka K. for her invaluable help, guidance and friendship in all our shared scientific endeavors. Terhi, Michael, Tanja H., Miia T., Andrey, Denis, Veli-Matti, Tuomas T., Wolf, Aino, Katja P., Seppo, Gabi, Marius and Markus are acknowledged for their important contributions to various aspects of the VEGF-B project. Special thanks go to Krista and Emmi for their friendship and for helping me stay sane with regular morning chats, as well as to Kati, Kirsi, Anita, Maija H., Ville and Harri for cathartic discussions over lunch. Marie and Marianna are thanked for friendly and cheerful discussions in the office, and Camilla, Marja, Paula and Gabi for diverting conversations during long days in the animal room.

Tapio is thanked for his unrivaled lab managing skills and for being available to help with any problem in the lab. I am also grateful to Katja S., Kirsi, Tanja L., Laura, Karita, Linda, Kaisa M., Seija, Ulla and Päivi for their professional assistance, as well as to the expert staff at the Biomedicum Imaging Unit and Meilahti and Ruskeasuo animal facilities. Miia P., Samu, Marie, Tuomas L., Marianna, Riikka P. and Kaisa S. are thanked for their administrative help.

My dearest friends Bettina and Anna are thanked for their kindness and patience, as well as for many supportive discussions over the years.

I dedicate this thesis to my mother, who I cannot thank enough for her support and without whom none of this would have been possible. I am sincerely thankful to my siblings Anna and Kristian for coping with stressful Christmas vacations, as well as to my father for helpful advice and many happy memories. I am also truly grateful to my grandmother for her love and devotion.

Finally, my dearest Marko, thank you for your untiring support, love and understanding and for making me feel at ease even during the most difficult and stressful times. I love you.

I have been financially supported by grants from the Biomedicum Helsinki Foundation, Finnish Foundation for Cardiovascular Research, Finnish Medical Foundation, Emil Aaltonen Foundation, Finnish Cardiac Society, Finnish Angiology Society, Orion-Farmos Research Foundation, Finnish Cultural Foundation, Finska Läkaresällskapet, Nylands Nation, Paulo Foundation, Maud Kuistila Memorial Foundation, Ida Montin Foundation, Aarne Koskelo Foundation, Oskar Öflund Foundation, Waldemar von Frenckell Foundation, and the Aarne and Aili Turunen Foundation, which are sincerely acknowledged.

Helsinki, November 2013

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